

GenCore version 4.5
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OM n clec - nucleic search, using sw model

Run n: June 2, 2000, 08:56:29 ; Search time 5907.01 Seconds
(without alignments)
2750.176 Million cell updates/sec

Title: US-09-284-180-1
Perf ct score: 4008

Sequence: 1 gccgagccgcgcagtagc.....aaaaaaaaaaaaaaaaaaaa

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Search: 4857316 seqs, 2026611650 residues

Total number of hits satisfying chosen parameters: 9714632

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

EST:
1: em_est1:
2: em_est2:
3: em_est3:
4: em_est4:
5: em_est5:
6: em_est6:
7: em_est7:
8: em_est8:
9: em_est9:
10: em_est10:
11: em_est11:
12: em_est12:
13: em_est13:
14: em_est14:
15: em_est15:
16: em_est16:
17: em_est17:
18: em_est18:
19: em_est19:
20: gb_est1:
21: gb_est2:
22: gb_est3:
23: gb_est4:
24: gb_est5:
25: gb_est6:
26: gb_est7:
27: gb_est8:
28: gb_est9:
29: gb_est10:
30: gb_est11:
31: gb_est12:
32: gb_est13:
33: gb_est14:
34: gb_est15:
35: gb_est16:
36: gb_est17:
37: gb_est18:
38: gb_est19:
39: gb_est20:
40: gb_est21:
41: gb_est22:
42: gb_est23:
43: gb_est24:

44: gb_est25:
45: gb_est26:
46: gb_est27:
47: gb_est28:
48: gb_est29:
49: em_est20:
50: em_est21:
51: em_est22:
52: gb_est30:
53: gb_est31:
54: gb_est32:
55: em_est23:
56: em_est24:
57: em_est25:
58: em_est26:
59: gb_est33:
60: gb_est34:
61: gb_est35:
62: gb_est36:
63: gb_est37:
64: gb_est38:
65: em_est27:
66: em_est28:
67: em_est29:
68: em_est30:
69: gb_est39:
70: gb_est40:
71: gb_est41:
72: gb_est42:
73: gb_est43:
74: gb_est44:
75: em_est32:
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77: em_est34:
78: em_est35:
79: gb_est45:
80: gb_est46:
81: gb_est47:
82: gb_gss1:
83: gb_gss2:
84: gb_gss3:
85: gb_gss4:
86: em_gss1:
87: em_gss2:
88: em_gss3:
89: em_gss4:
90: gb_gss5:
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95: gb_gss8:
96: gb_gss9:
97: em_gss7:
98: em_gss8:
99: gb_gss11:
100: gb_gss10:
101: em_gss9:
102: em_gss10:
103: em_gss11:
104: em_gss12:
105: gb_gss12:
106: gb_gss13:
107: gb_gss14:
108: gb_gss15:
109: gb_gss16:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Length	DB	ID	Description
1	437.2	10.9	466	69	AM123399	AM123399 UT-M-BH2.
2	405.2	10.1	434	69	AM123577	AM123577 UT-M-BH2.
3	383.6	9.7	503	34	AA459837	AA459837 zxs05g12.r
4	293.6	7.3	517	22	RS48487	RS4837 y978412.r1
5	289.6	7.2	337	20	245339	245339 HSC2MG091.n
6	287.4	7.2	364	20	T09073	T09073 EST06966.tn
7	284.4	7.1	376	81	AM46751	AM46751 77209.MAR
8	283.8	7.1	437	73	H24181	H24181 ym55f02.r1
9	281.6	7.0	347	22	H10823	H10623 ym08g07.r1
10	258	6.4	379	42	AM158284	AM158284 udc3h09.r
11	211.8	5.3	305	69	AM122335	AM122335 UT-M-BH2.
12	193.6	4.8	592	106	AO352219	AO352219 CTTB-ET1-
13	150.8	3.8	208	81	AM46702	AM46702 77141.MAR
14	138.8	3.5	257	72	AV329323	AV329323 AV329323
15	118.2	2.9	490	45	AI365650	AI365650 ap20h08.x
16	111.4	2.8	619	64	AL118624	AL118624 DFE2P761F
17	110.2	2.7	232	80	AM346693	AM346693 29273.MAR
18	110.2	2.7	232	80	AM346698	AM346698 29272.MAR
19	109	2.7	212	20	Z42773	Z42773 HSC0FE021.n
20	102.4	2.6	463	74	AM206442	AM206442 UT-H-B11-
21	100.8	2.5	558	44	AI313725	AI313725 HA335.Hu
22	99.2	2.5	395	44	AI289278	AI289278 gw37206.x
23	98.6	2.5	359	20	T35785	T35785 EST91372.Hu
24	97.8	2.4	442	26	W39580	W39580 zc20c05.r1
25	94.8	2.4	350	20	Z43006	Z43006 HSC10E011.n
26	94.4	2.4	450	70	AM148766	AM148766 x102h03.x
27	87.8	2.2	427	47	AI533743	AI533743 th18d02.r1
28	86.6	2.2	453	22	H08892	H08892 y18bd02.x
29	85	2.1	448	61	AI858820	AI858820 w135908.x
30	85	2.1	448	61	AA523537	AA523537 nq30e03.s
31	78.4	2.0	591	34	AA523537	AA523537 nq30e03.s
32	76.8	1.9	942	69	AM078986	AM078986
33	75.6	1.9	442	48	AI555178	AI555178 UT-R-C2P-
34	75.6	1.9	638	79	AM245910	AM245910 2822868.5
35	74.6	1.9	395	26	W52192	W52192 zc46g02.s1
36	71.8	1.8	469	42	AI141990	AI141990 ool79410.x
37	69.4	1.7	338	38	AA761030	AA761030 nm08h08.s
38	69.4	1.7	697	69	AM134401	AM134401 f118h09.Y
39	69	1.7	519	94	AO925155	AO925155 RCT1-23-3
40	69	1.7	737	109	AO643575	AO643575 RPT13-EC
41	68	1.7	479	82	FR0003554	287337 F_rubirdipes
42	68	1.7	802	69	AM128036	AM128036 f106a12.Y
43	67.8	1.7	1104	82	CNS0041E	AL078534 drosoph11
44	67.4	1.7	1203	82	CNS00737	AL067347 drosoph11
45	67.4	1.7	600	83	FR0042485	AL129977 Eugu.rubr
46	67	1.7	449	47	AI545466	AI545466 EB81902.x

RESULT	1
AM123399	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTORS	
TITLE	
JOURNAL	
MEDIA	
COMMENT	

AM123399 466 bp mRNA EST 22-OCT-1999
 UT-M-BH2.1-apj-a-04-0-UI.s1 NIH_BMAP_M.S3.1 Mus musculus cDNA clone
 UT-M-BH2.1-apj-a-04-0-UI.3', mRNA sequence.
 AM123399
 AM123399.1 GI:6098929
 EST.
 house mouse.
 Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 466)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 97044477
 On Mar 10, 1998 this sequence version replaced gi:2948620.
 Contact: Chin, H

National Institute of Mental Health
6001 Executive Blvd. Room 7N-7150, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 3706
Fax: 301 443 9890
Email: mestr@mail.nih.gov
Oligo-dT track not found. Not i site shown in beginning of sequence
is likely internal to the message. CDNA Library preparation: M.B.
Soares Lab Clone distribution: NIH BMAP CDNA clones will be made
available by the means that is soon to be determined. When NIH
determines the means for distribution of the BMAP CDNA clones, this
record will be updated accordingly when that means is determined.
Seq primer: M13 forward
Seq primer: M13 reverse
COLTA-No.

FEATURES	Location/Qualifiers
source	1. . 466

/organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UI-M-BH2.1-apj-a-04-0-01"
 /clone_id="NIH_BMAP_M.S3.1"
 /dex_stage="27-32 days"
 /lab_host="DH10B (Life Technologies)"
 /note=Vector: pT713D-Pac (Pharmacia) with a modified
 polylinker; Site-1: Not I; Site-2: Eco RI; The
 NIH_BMAP_M.S3.1 library is a subcloned library of a
 series, ultimately derived from a mixture of individually
 tagged normalized libraries from ten regions of the mouse
 brain (cerebellum, brain stems, olfactory bulbs,
 hypothalamus, cortex, amygdala, basal ganglia, pineal
 gland, striatum, hippocampus) after a series of
 subtractions to reduce the representation of cDNAs from
 which ESTs had already been generated. The following
 serially subcloned libraries were generated in this
 process: NIH_BMAP_M.S3.1, NIH_BMAP_M.S2, NIH_BMAP_M.S1.
 The subcloned library (NIH_BMAP_M.S3.1) was constructed
 as follows: PCR-amplified cDNA inserts from NIH_BMAP_M.S2
 clones from which 3' ESTs had been derived was used as a
 driver in a hybridization with the NIH_BMAP_M.S2 library
 in the form of single-stranded circles. The remaining
 single-stranded circles (subcloned library) was purified
 by hydroxyapatite column chromatography, converted to
 double-stranded circles and electroporated into DH10B
 bacteria (Life Technologies) to generate the
 NIH_BMAP_M.S3.1 library. This procedure has been
 previously described (Bonaldo, Lennon and Soares, Genome
 Research 6:791-806, 1996)
 TAG_Lib=NIH_BMAP_M.S3.1
 TAG_Tissue=pineal-glands
 TAG_SEQ=CAGAC"

BASE COUNT	95 a	139 c	120 g	112 t
ORIGIN				

Query Match	10.9%	Score 437.2	DB 69	Length 466
Best Local Similarity	96.1%	Pred. No. 8.4e-89		
Matches 448	Conservative 0	Mismatches 18	Indels 0	Gaps 0
QY 189	cgagcgcgctcccccgcctcagtcgtgccagaacctgcctgcacatctccgagcgtgacctcta	248		
Db 1	CGGCGCGCTCCCGCGTCGTGGCCAGAACCTCCCTGCCATCCGAGCGCTGACTCTTA	60		
QY 249	tctaccgcggtttccagcgcgtctcatalagtaaatctatctcctctccttggtagtctgc	308		
Db 61	TCTACCCGGTTTCGGGCCCTCTCAACGTAAATTAATCTCTCTCTCTCGTGGGATCCTGC	120		
QY 309	ctcccaacaccttaccgtctcgtgtcacggatagatctctgctttaaaccctccctcttc	368		
Db 121	TTTCACACACTTACGTCGCGTCACACGGACAGCATCTTCGCTTAACCTGCCCTTCTC	180		
QY 369	tggggaaaagacccccgaagatcgcactgtgatgtaccctcgagagactcaacagacgaactcag	428		
Db 181	TGGGAAAAGCCTTGGAAGGATCGACTGGATGTGTCGCCGAGACTCACAGACGAACCTTAG	240		

429 gaagaaagcgaagaagaagcgaatgcacatttaccagattctcgccatgca 488
 241 GAAGAAAGCAGAAAGAGAGAGATGTCACAAATTTATCCAGATTCGCGCATGCCAA 300
 489 tgccttaccctcctcgaagtcgagccttcgtttatccgaagtcgaggtatga 548
 301 TGCTCTCACTCCTCAGAGTGTGACCTTGCTTTTATCCAGATTCGCGCATGCCAA 360
 549 tgccttaccctcctcgaagtcgagccttcgtttatccgaagtcgaggtatga 608
 361 TGTGTCCAGTTTCCAGAGCTTGAAGACATTGAGAGTGGCGGGAATGTCCTTTGA 420
 609 gccagctcaagctcagcagctgtatgctgctggcgctcctctac 654
 421 GCCAGCTCAACGCTCAGCTGTATGCTGGGGCGCTCTCTAC 466

RESU T 2
 AM12 577
 LOCUS: AM123577 434 bp mRNA EST 22-OCT-1999
 DEFINITION: UI-M-BH2.1-ap1-a-04-0-UI.S1 NIH_BMAP_M.S3.1 Mus musculus cDNA clone
 ACCESSION: AM123577
 VERSION: AM123577.1 GI:6099107
 KEYWORDS: EST.
 SOURCE: house mouse.
 ORIGIN: Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 434)
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 97044477
 On Mar 10, 1998 this sequence version replaced gi:2948806.
 Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: MEST@mail.nih.gov
 Oligo-dT track not found, Not I site shown in beginning of sequence
 is likely internal to the message. cDNA Library Preparation: M.B.
 Soares Lab Clone distribution: NIH BMAP cDNA clones will be made
 available by the means that is soon to be determined. When NIH
 determines the means for distribution of the BMAP cDNA clones, this
 record will be updated accordingly when that means is determined.
 Seq primer: M13 Forward
 POLY-A-NO.

FEAT RES
 source

Location/Qualifiers
 1. 434
 /organism="Mus musculus"
 /strain="CS7BL/6J"
 /db_xref="taxon:10090"
 /clone="UI-M-BH2.1-ap1-a-04-0-UI"
 /lab_host="NIH_BMAP_M.S3.1"
 /dev_stage="27-32 days"
 /note="Vector: pUT3D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; The
 NIH_BMAP_M.S3.1 library is a subtracted library of a
 series, ultimately derived from a mixture of individually
 tagged normalized libraries from ten regions of the mouse
 brain (cerebellum, brain stems, olfactory bulbs,
 hypothalamus, cortex, amygdala, basal ganglia, pineal
 gland, striatum, hippocampus) after a series of
 subtractions to reduce the representation of cDNAs from
 which ESTs had already been generated. The following
 serially subtracted libraries were generated in this
 process: NIH_BMAP_M.S3.1, NIH_BMAP_M.S2, NIH_BMAP_M.S1.

The subtracted library (NIH_BMAP_M.S3.1) was constructed
 as follows: PCR-amplified cDNA inserts from NIH_BMAP_M.S2
 clones from which 3' ESTs had been derived were used as a
 driver in a hybridization with the NIH_BMAP_M.S2 library
 in the form of single-stranded circles. The remaining
 single-stranded circles (subtracted library) was purified
 by hydroxyapatite column chromatography, converted to
 double-stranded circles and electroporated into DH10B
 bacteria (Life Technologies) to generate the
 NIH_BMAP_M.S3.1 library. This procedure has been
 previously described (Bonaldo, Lennon and Soares, Genome
 Research 6:791-806, 1996)
 TAG: NIH_BMAP_M.S3.1
 TAG: TISSUE=pineal glands
 TAG: SEQ=CCATC
 BASE COUNT 90 a 130 c 109 g 105 t
 ORIGIN

Query Match 10.1%; Score 405.2; DB 69; Length 434;
 Best Local Similarity 95.9%; Pred. No. 1.4e-81;
 Matches 416; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
 189 cggccgcgtcccccgcagtcagtcgacgaagcctgctgcccacatccgaggtgactcta 248
 1 CGGCGCGCTCCCGCGCTCGTGGCCAGACCTCCGCTCCAGAGCTGACTCTTA 60
 249 tctaccgcgtttgcagcgtctcactacgaattactctctcttctgtgactctgc 308
 61 TCTCACCCTGTTGCGGCCCTCATAGTACATTAATCTCTCTCTGTTGATCTCTGC 120
 309 ctccacacacatttaagtcggtgacggaggaagatcttgccttaaccctcccttc 368
 121 TTCACACACTTACGCTGCGTGCACGACGACGATCTTCCTTAACTCCGCTTCTC 180
 369 tggggaagaccgccgaagagatcgatgattctctctgagactacagagaagctgag 428
 181 TGGGGAAGAGCTCGAAGAGATCGACTGATGTGCTCCAGACTACAGACGAAGTCTAG 240
 429 gaagaaagcgaagaagaagcgaatgtcacatttaccagattctcgccatgca 488
 241 GAAGAAAGCAGAAAGAGAGAGATGTCACAAATTTATCCAGATTCGCGCATGCCAA 300
 489 tgccttaccctcctcgaagtcgagccttcgtttatccgaagtcgaggtatga 548
 301 TGCTCTCACTCCTCAGAGTGTGACCTTGCTTTTATCCAGATTCGCGCATGCCAA 360
 549 tgccttaccctcctcgaagtcgagccttcgtttatccgaagtcgaggtatga 608
 361 TGTGTCCAGTTTCCAGAGCTTGAAGACATTGAGAGTGGCGGGAATGTCCTTTGA 420
 609 gccagctcaagcgt 622
 421 GCCAGCTCAACGCT 434

RESULT 3
 LOCUS: AA459837 503 bp mRNA EST 09-JUN-1997
 DEFINITION: z550912.1 Soares testis NHT Homo sapiens cDNA clone IMAGE:795718
 5' similar to TR:G554328 G854328 SEAHORIN C, mRNA sequence.
 ACCESSION: AA459837
 VERSION: AA459837.1 GI:2184744
 KEYWORDS: EST.
 SOURCE: human.
 ORGANISM: Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 503)
 REFERENCES
 1 Haller, L., Allen, M., Bowles, L., Dubuque, J., Gelsel, G., Jost, S.,
 Kucaba, T., Lacy, M., Lennon, G., Marra, M., Martin, J.,
 Moore, B., Schellenberg, K., Stepien, M., Tan, F., Theising, B.,
 White, Y., Wylie, T., Waterston, R. and Wilson, R.

TIJ.E
JOURNAL
COMMENT
Washu-Merck EST Project 1997
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1392936.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from AmerSham
High quality sequence stop: 459.

FEATURES

source

1. 503
/organism="Homo sapiens"
/db_xref="GDB:6039163"
/db_xref="taxon:9606"
/clone="IMAGE:795718"
/clone_lib="Soares_testis_NH"
/sex="male"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5].
TGTACCAATCTGAACTGGAGGAGCGGCCCAATTTTCTTTTCTTTT 3']
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT
ORIGIN

Query Match 9.7%; Score 386.8; DB 34; Length 503;
Best Local Similarity 88.2%; Pred. No. 2.2e-77;
Matches 443; Conservative 0; Mismatches 57; Indels 2; Gaps 2;

1387 gactatcagagtcgtggtccacaggtgtacacagctctcagggaaagatatgacgtg 1446
1 GCCTATCTCAGATCGTGGCCACCA-GGTACACAGCCTCTCAGGGAAGATGATGCTG 59
1447 ctctaccctggagaca-gaggatggacacctccacagggctgtgacatcggagctacgt 1505
60 CTCTACTCTGGGACATGAGATGACACCTCCACCGAGCTGCGAGCTCAGCT 119
1506 cagtgtcctggagatctggtctgtccagaaacacacagcggttagagagcatgaatt 1565
120 CACCGTTCTTGAAGATCTGGCTTATTCACAGACCCACAGCTTGAACATGAAATT 179
1566 gtaccacagatctgctcctgtgtggtcccaactgtgaggtgtacacaaagtgacacagca 1625
180 GTACACAGATGGCTCTGTTGGCTCCGTACTAGAGTGTACACAAAGTGAATACACCAA 239
1626 ctgtgacgctctccagagctgtcgtgaggtatccgtgcccaggaaccgctgtgagcctg 1685
240 CTGTGGCCGCTCTCAGAGCTGCTCAGAGTGCATCTGCGCCAGACCCACATCTGTGCTG 299
1686 gaggctcggagctgagctgtgtgtgcccagcgcgaggaacacggagtggttcaaga 1745
300 GACCTTCGGCTGATGATGATGTGTGGCCATGCGGGGAGACCGGAGGTGGTCCCAAGA 359
1746 tatagagtcagcgatgtctctctctgtgtccaaagaaacccctggaacatcccgtagt 1805
360 CAAAGATGACGACATCTCCCTTTGTGTCTCTAGAGACCTCGAAGAGCTCCAGACTG 419
1806 gtttgaagtcgggtgtctactgtgtggcacaagtcgtccatgttcccccagttctgc 1865
420 GTTTGAAGTCCCGTGGCTACAGCTCGGCATGTGTTCTTCCCATGTTCTCAAGCTCAGC 479

QY 1866 ctggacatcctgtgtgtgac 1887
Db 480 ATGGCATCTCTGTGTGGC 501

RESULT 4
LOCUS R54387
DEFINITION R54387
R54387
IMAGE:39491 5' similar to SP:A49069 A49069 COLLAPlIN -, mRNA
sequence.
ACCESSION R54387
VERSION R54387.1 GI:816289
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 517)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Woldmann, P. and
Wilson, R.
The Washu-Merck EST Project
Unpublished (1995)
CONTACT: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
Insert Size: 2134
High quality sequence stops: 99 Source: IMAGE Consortium, LNL. This
clone is available royalty-free through LNL; contact the IMAGE
Consortium (info@image.llnl.gov) for further information.
Insert Length: 2134 Std Error: 0.00
Seq primer: M13Rpi
High quality sequence stop: 99.

FEATURES

source

1. 517
/organism="Homo sapiens"
/db_xref="GDB:412032"
/db_xref="taxon:9606"
/clone="IMAGE:39491"
/clone_lib="Soares Infant brain INTB"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: whole brain; Vector: Lambda B4; Site 1: Not
I; Site 2: Hind III; 1st strand cDNA was primed with a Not
I - oligo(dT) primer [5].
AAGTGAAGAAATTCGGGCGCGCGGGAATTTTCTTTTCTTTT 3']
Double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the Lambda B4 vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT
ORIGIN

Query Match 7.3%; Score 293.6; DB 22; Length 517;
Best Local Similarity 85.6%; Pred. No. 2.9e-56;
Matches 370; Conservative 0; Mismatches 55; Indels 7; Gaps 4;

QY 1127 gaccacaagacatccggagtgatgtatgtcccttagagagctaaacatgactga 1186
Db 1 GACCAACAGACATTCGGAAGTGTCTTAATGTCCTTCAGAGACTAAACATGACTGA 60
QY 1187 acagaggaactgctctcatgagcaaacagaggtgccccaagcagacctgagagtgatcg 1246
Db 61 ACAGAGACTGCGCTCGTGGTGAATGATGTGCCAGCCAGACACTGAGATGATCA 120

```

QY 1247 ccaacaacatgaagctccagcagtttgatctctactctccctgcagacccgctgctca 1306
DB 121 ccaacacatgaagctccgacacgttgctctctctctccctgcagacccgctgctca 180
QY 1307 ccttatacagaagacccctctcatgagagccgctgtctcccgctgagccgcccc 1366
DB 181 ccttctccgggagacacccactatgacagcagcagctgttccagctgagccgcccc 240
QY 1367 tctgtgctactacagatagacccatctcagagctgctgagccagaggtgacccgctct 1426
DB 241 tctgtgctactacagatagacccatctcagagctgctgagccagaggtgacccgctct 300
QY 1427 cagggaagaataatgacgtgctctaccc- gggagacagagat- ggaacccctccacggc 1484
DB 301 cagggaagaataatgacgtgctctaccc- gggagacagagat- ggaacccctccacggc 360
QY 1485 tctgagcatt- ggaagctcagctcagagctgctgagga- -tctgagcctgtctccagaa 1539
DB 361 agtgcgattcggagctcagctcagagctgctgagga- -tctgagcctgtctccagaa 420
QY 1540 ccacagccggtt 1551
DB 421 TCACAGNCAGTT 432

RESULT 5
LOCUS 245329 337 bp mRNA EST 14-NOV-1994
DEFINITION HSCMG091 normalized infant brain cDNA Homo sapiens cDNA clone
ACCESSION C-2mg09, mRNA sequence.
VERSION 245329.1 GI:574541
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AU HORS 1 (bases 1 to 337)
Auffray,C., Behar,G., Bols,F., Bouchier,C., da Silva,C.,
Devignes,M.D., Duprat,S., Houllatte,R., Jumeau,M.N., Lamy,B.,
Lorenzo,F., Mitchell,H., Marille-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Kabakchis,C. and Tessier,A.
IMAGE: molecular integration of the analysis of the human genome
and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
CONTACT: Genethon
Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr
Single read
Genexpress_library_id: C; Genexpress_sequence_id: y1c-2mg09
Seq primer: (-21)M13-universal.
FEATURES
Source
1..337
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="normalized infant brain cDNA"
/sex="Female"
/tissue_type="total brain"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site: 1: HindIII;
Site: 2: NotI; sex=Female; dev_stage=3 months old.
Isolate=muscular atrophy patient; tissue_type=total
brain; total mRNA was oligo-(dt) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B. Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:"

```

```

BASE COUNT 81 a 106 c 82 g 67 t 1 others
ORIGIN
Query Match 7.2% Score 289.6; DB 20; Length 337;
Best Local Similarity 91.1%; Pred. No. 2e-55;
Matches 307; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1126 ccacccaagaatccagcagctgctgaaagcttcccttagagagctaaacatgactgc 1185
DB 1 ccacccaagaatccagcagctgctgaaagcttcccttagagagctaaacatgactgc 60
QY 1186 aacagggagactcctgtcactgacaaagaggtgcccagccagacactgagagtgatc 1245
DB 61 AACAGGAGACTCCCTGTCAGTATGATGTCACCACTGAGAGAGTGCATC 120
QY 1246 gccacaacatgaagctccagcagctgctgaaagcttcccttagagagctaaacatgactgc 1305
DB 121 ACCAACACATGAAGCTCCGACACTTGGCTCATCTCTCCCTGCTGACCGCTACTC 180
QY 1306 accctatcagaagacacccctctcagacagccgctgtcccgctgacggccgcccc 1365
DB 181 ACCTTCATCCGGAGACACCCACTCATGACAGCCAGTGTTCAGCTGATGCCCC 240
QY 1366 ctgctgtgctactacagatagacccatctcagagctgctgagccagaggtgacccgctc 1425
DB 241 CTGCTGTGCTACTACATGATGCTCAGCTATCTCAGAGTGTGTCACAGGCTGACGACCTC 300
QY 1426 tcagggaagaataatgacgtgctctacccgagagacg 1462
DB 301 TCAGGGAAGAAGTATGATGCTCTACCTGCGGACG 337

RESULT 6
LOCUS T09073 364 bp mRNA EST 03-AUG-1993
DEFINITION EST06966 Infant Brain, Bento Soares Homo sapiens cDNA clone HIB071
5' end, mRNA sequence.
ACCESSION T09073
VERSION T09073.1 GI:390101
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AU HORS 1 (bases 1 to 364)
Adams,M.D., Soares,M.B., Kerlavage,A.R., Fields,C. and Venter,J.C.
Rapid cDNA sequencing (expressed sequence tags) from a
directionally cloned human infant brain cDNA library
Nature Genet. 4, 373-380 (1993)
94004965
CONTACT: Adams, MD
The Institute for Genomic Research
932 Clopper Road, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: mdadams@tigr.org
Seq primer: M13 Reverse.
FEATURES
Source
1..364
/organism="Homo sapiens"
/db_xref="ATCC (Inhost):85555"
/db_xref="taxon:9606"
/clone_1lb="HIB071"
/clone_1lb="Infant Brain, Bento Soares"
BASE COUNT 70 a 100 c 106 g 85 t 3 others
ORIGIN
Query Match 7.2% Score 287.4; DB 20; Length 364;
Best Local Similarity 86.5%; Pred. No. 6.5e-55;
Matches 315; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

```

QY 1561 aaattgtaccagatttgctctctgtgtggctccactactagatgagacaaagttaacacc 1620
 |||||
 Db 1 AAATTGTACCAACAGCTGCTCTGTTGGCTCCGTTACTGAGTACACAGTGAATACA 60
 |||||
 QY 1621 agcaactgtgcccgtcccaagactgtctgagatgtatccctggcccgagaccctgtgtgc 1680
 |||||
 Db 61 ACNACTGTGGCCCTCTCCAGAGCTGCTCAGAGTGACATCCGCGCCAGACCCAGTCTGT 120
 |||||
 QY 1681 gctcgtgagctcccgctgtgatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1740
 |||||
 Db 121 GCCGTGAGCTCCCGCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
 |||||
 QY 1741 caagatatagagtcagcagcagatgtctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1800
 |||||
 Db 181 CAACACATAGATGACGAGATGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
 |||||
 QY 1801 gtatgt 1860
 |||||
 Db 241 GTAGT 300
 |||||
 QY 1861 tctgctgtgagctctgt 1920
 |||||
 Db 301 TCAGCAGGAGGATCCTGT 360
 |||||
 QY 1921 aggg 1924
 |||||
 Db 361 CGGG 364

RESULT 7

LOCUS AM436751 376 bp mRNA EST 14-FEB-2000
 DEFINITION 77209 MARC 2Pig Sus scrofa cDNA 5', mRNA sequence.
 ACCESSION AM436751
 VERSION AM436751.1 GI:6972057
 KEYWORDS EST.
 SOURCE pig.
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Cetartiodactyla; Suidae; Sus.
 1 (bases 1 to 376)
 Fahnenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
 Stone, R.T., Heaton, M.P., Grosche, W.M., Bennett, G.A. and Keele, J.W.
 Design and use of two pooled tissue normalized cDNA libraries for
 EST discovery in swine
 Unpublished (2000)
 On Jul 9, 1999 this sequence version replaced gi:5435515.
 CONTACT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4366
 Email: smitht@mail.marc.usda.gov
 Single pass sequencing. Bases called and trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 20
 and -minmatch 12 options.
 PCR PRIMERS
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCTCCAGTCACGACG
 Plate: 32 Row: A Column: 20
 Seq primer: ATTTAGGTGACACTATAG.
 Location/Qualifiers
 1..376
 /organism="Sus scrofa"
 /db_xref="taxon:9823"
 /clone_id="MARC 2Pig"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPORT6, site_1: XbaI; site_2: XhoI;
 library made from pooled tissue from testis, ovary,
 endometrium, hypothalamus, pituitary, and placenta."

REFERENCE
 AUT HORS
 TITLE
 JOURNAL
 COMMENT

FEATURE RES

BASE COUNT 60 a 129 c 116 g 71 t

ORIGIN

Query Match 7.1%; Score 284.4; DB 81; Length 376;
 Best Local Similarity 86.9%; Pred. No. 3,1e-54;
 Matches 325; Conservative 0; Mismatches 46; Indels 3; Gaps 1;
 QY 2032 agccaagggggagacccttaaacccgggcccacacgctgtgtgtgtgtgtgtgtgtgtgt 2091
 |||||
 Db 2 AGCCAGAGGGGGGCCCCCAACCCGGGCTCACAC--AGTGGGGCCGAGTGGAGGCTTC 58
 |||||
 QY 2092 ctctcgt 2151
 |||||
 Db 59 TTCTGGGGGTTCTTGACAGATCCCTGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 118
 |||||
 QY 2152 cggcagcagagggagct 2211
 |||||
 Db 119 CAGGACAGAGGAGGCTTCTGCTAGACACAGTGGGCTTGACCTGGGGGTCACAGCA 178
 |||||
 QY 2212 tctgt 2271
 |||||
 Db 179 TCCGGGACACAGCTACAGCCAGGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 238
 |||||
 QY 2272 cccctgt 2331
 |||||
 Db 239 CCCTGGCCCTGGCCAGAGAGGGGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 298
 |||||
 QY 2332 gattctgtcccaagccagccacatccgctcactgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2391
 |||||
 Db 299 GATCCTTGCCCGAGCCAGCCACATCGGTGACGGGGGCTCTCTAGACACATGTGAT 358
 |||||
 QY 2392 gagaccccatccta 2405
 |||||
 Db 359 GAACGCTCATCTA 372

RESULT 8

LOCUS H24181 437 bp mRNA EST 06-JUL-1995
 DEFINITION ym55f02.r1 Soares Infant brain INTB Homo sapiens cDNA clone
 IMAGE:52280 5' similar to SP:A49069 A49069 COLLAPSLIN - ; mRNA
 sequence.
 ACCESSION H24181 GI:892876
 VERSION H24181
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 437)
 Hillier, L., Clark, N., Dubuque, T., Elliston, R., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
 Trevasakis, E., Waterston, R., Williamson, A., Woldmann, P. and
 Wilson, R.
 The WashU-Werck EST Project
 Unpublished (1995)
 CONTACT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 Insert Size: 1989
 High quality sequence stops: 310 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 1969 Std Error: 0.00
 Seq primer: MJ3P1
 High quality sequence stop: 310.
 Location/Qualifiers
 1..437
 /organism="Homo sapiens"

TITLE

JOURNAL
 COMMENT

FEATURES

source
 1..437
 /organism="Homo sapiens"

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/db_xref="GDB:425216"
/db_xref="taxon:3606"
/clone="IMAGE:52280"
/clone_lib="Soares Infant brain INIB"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: whole brain; Vector: Latmid BA; Site_1: Not I; Site_2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5', AACGGAAGAATTCGCGCCGACGAAATTTTTTTTTTTT 3'); double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the latmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      105 a      122 c      112 g      95 t
ORIG N

```

Query Match	Similarity	Score	DB	Length
Query Match	Similarity	Score	DB	Length
1	88.8%	283.8	23	437
318	Conservative	0	Mismatches	38
			Indels	2
			Gaps	1

```

FEATURES
source
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
Insert Site: 1985
High quality sequence stops: 198
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1985 Std Error: 0.00
Seq primer: M13Rp1
High quality sequence stop: 198.
Location/Qualifiers
1..347
/organism="Homo sapiens"
/db_xref="db:419839"
/db_xref="taxon:9606"
/clone="IMAGE:47298"
/clone_id="Soares infant brain INIB"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DR10B (ampicillin resistant)"
note="Organ: whole brain: Vector: Lambda BA: Site:1: Not
I: Site:2: Hind III: 1st strand cDNA was primed with a NOB
I - oligo(dT) primer [5'
AAGCGAAGAAATTCGCGCCGACGGAATTTTTTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the Lambda BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT
82 a 105 c 87 g 67 t 6 others
ORIGIN

```

Query Match	7.0%	Score 281.6	DB 22	Length 347
Best Local Similarity	90.1%	Pred. No. 1.3e-53		
Matches 299	Conservative 0	Mismatches 33	Indels 0	Gaps 0
QY 1127	gaccccaagacacccgggcagtcgtgaa1tgccttttagaagctaaacatgactgca	1186		
Db 1	GACCACAGAGACTTGTGGACAGTGCATGTGGTCCCTTCAGAGAACTAAACATGACTGCA	60		
QY 1187	acaaggagactgcctctcattgagcaaaagagtgcgccagcccaagaccttggagagtgatcg	1246		
Db 61	ACAGAGGACTGCTGCTGCGACATGATGATGTGCCACCCAGACCTGGAGAGTGCATCA	120		
QY 1247	ccaacaaatgaagttccagcaggtttgatctctactcttcctgtgccaaacggcggtcca	1306		
Db 121	CCANCAACATGAGTGTCCGGCATTGTGCTATCTCTCTCCTGCTACACGCGTACTCA	180		
QY 1307	ccattatagagagaccacctctcatgagcaagcccggtgtccggcgtgacagccggcccc	1366		
Db 181	CCTTATATCCGGGACCAACCCACTCATGAGCAGGCCAGTGTTCACGCTAATNCCACCCCC	240		
QY 1367	tgcgtgtcactacagatacaagccctatcccaagatcgttggcccaacagagg1gaacagcctct	1426		
Db 241	TGCTGCTCAGTACAGATACAGCCTATCTCAGAGTGTGTGGCCACAGGGGAGACCAAGNCGT	300		
QY 1427	cagggaagaatatatgacgtgtcctctcactcctgggg	1458		
Db 301	CAGGNAAGAGATGATGATGTGCTCTACCTGGGG	332		
RESULT 10				
LOCUS A1158284	379 bp	mRNA	EST	30-SEP-1998
DEFINITION uc23h09.t1 Soares_thymus_2NBMT Mus musculus CDNA clone				
IMAGE:1446785 5' / mRNA sequence.				
ACCESSION A1158284				
VERSION A1158284.1	GI:3686753			
KEYWORDS EST.				
SOURCE house mouse.				


```

/tissue_type="pooled"
/lab_host="DH10B"
/notice="Vector: PCMV_SPORT6; Site 1: xbaI; Site 2: xhoI
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT      36 a      64 c      73 g      35 t
ORIGIN

```

Query Match	3.8%;	Score 150.8;	DB 81;	Length 208;
Best Local Similarity	85.7%;	Pred. No. 4.6e-24;		
Matches 180;	Conservative 0;	Mismatches 27;	Indels 3;	Gaps 1;

2032 agccagcgggagacccctcaaacccggcgcccacaacgcgttgagggggtgatgtgtgcttc 2091
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2 AGCCACGGGGGCCCCCAAGCGGGCTCACAC--AGTGGGGGCCCGGACTTGCAAGCCTTC 58

2092 ctcctcgtgtctctctgcagcatcccccactcctccctccgattgttcgcgtcagcagcgt 2151
|||||
59 TTCCTGGGGGTTCTTGCACATCCCTGACTCTTCTCCGATTGCTGGGCGCAGCAGCGG 118

2152 cggcgacagaggagacttcctagctagagacaaggttggtcctagtatctggygcctccacct 2211
+ |||||
119 CAGCGACAGGGGACTTCTGGCTAGACAGCAAGTTGGCTTGACCTGGGGGTCCACGCA 178

2212 tcctggaccacaagctatagtcaggaccct 224
179 TCCGGACCAACAAGCTACAGCCAGGACCT 208

	AV329323	257 bp	mRNA	EST	11-NOV-1999
	AV329323		RIKEN full-length enriched adult male medulla oblongata		
	AV329323		Mus musculus cDNA clone 6330501j74.3' similar to AB021291 Mus		
			musculus mRNA for semaphorin W, mRNA sequence.		

AV329323 GI:6369375
AV329323.1
EST.

ORGANISM

EEFF ENCEE
AUI -IORS

TITLE
JOURNAL
NUMBER

Kaito, K., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusabe, M.,
 Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
 Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, Y.,
 Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugihara, Y.,
 Suzuki, H., Suzuki, H., Takahashi, F., Tateo, M., Tomihaga, N.,
 Tsunoda, Y., Watanishi, A., Watanabe, S., Yamamura, T., Yasunishi, A.,
 Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Kono, H., et al.)
 Unpublished (1999)
 On Dec. 20, 1995 this sequence version replaced gi:1133967.
 Contact: Yoshinide Hayashizaki
 Genome Exploration Research Group, Life Science Tsukuba Center,
 Genome Science Laboratory
 The Institute of Physical and Chemical Research (RIKEN), Genomic
 Science Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: +81-298-36-9013
 Fax: +81-298-36-9098
 Email: genome-research.riken.go.jp/
 URL: http://genome.riken.go.jp/
 Sasaki, N., Izawa, M., Watanishi, A., Ozawa, K., Tanaka, T.,
 Matsuyama, S., Carninci, P., Muramatsu, M., Okazaki, Y. and
 Hayashizaki, Y.
 Transcriptional sequencing: A method for DNA sequencing using RNA
 polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
 Itoh, M., Kitanai, T., Akiyama, Y., Shibata, K., Izawa, M., Kawai, J.,

Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y., and Hayashizaki, Y. Automated filtration-based high-throughput plasmid preparation system. *Genome Res.* 9 (5), 463-470 (1999).

Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303, 19-44 (1999).

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

Education/Qualifia

REFERENCE

FEATURES	Location/Qualifiers
source	1. . 257

```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="6330501J24"
/clone.lib="RIKEN full-length enriched, adult male medulla oblongata"

```

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/sex = male
/tissue_type = "medulla oblongata"
/dev_stage = "adult"
/lab_host = "hnu10a"
```

/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Institute, Ibaraki, Japan.

Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was

GAGAGAGAGAGATCCACAGACTCTTTTCTTTTTTTTNN 3'), cDNA was prepared by using trehalose thermo-activated reverse

transcriptase and subsequently enriched for full length cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adaptor of

sequence [5' GAGAGAGAGATTCTCGAGTATTAATTAATTAATCCCCCCCCCC
3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision

from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"

BASE COUNT	72 a	59 c	55 g	71 t
------------	------	------	------	------

	ORIGIN
0	0
1	1
2	2
3	3
4	4
5	5
6	6
7	7
8	8
9	9
A	A
B	B
C	C
D	D
E	E
F	F
G	G
H	H
I	I
J	J
K	K
L	L
M	M
N	N
O	O
P	P
Q	Q
R	R
S	S
T	T
U	U
V	V
W	W
X	X
Y	Y
Z	Z

Query match:	0.98	BLAST 2.2.0-rc2, 28/07/2001
Best Local Similarity	79.58%	Pred. No. 2.6e-21
Matches 202; Conservative	0; Mismatches 47;	Indels 5; Gaps 3;

Qy 3729 gggaccctcaaaccccaatgctcgtatgtctaaccccttccagtggaagttctgtctctgcttc 3788

QY 3789 cttgacagcagccgtgaactactcaagagtccccct-ggttggatgcccgtagctt 3847
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

3848 **tyagtagagatcttggcggtgcgtcatctaacctgacagcatatgacgttca-ttgtaaagt** 3906

DB: 124 TGAGTAGGATCTTTGGCAAGTAGTCTAACCTTAGGACATTTGGTTATTATATATAAAGTG 183

Db 184 GGGATATACCTACTTCGAGGGTGTCTCGAAGATCAACGAGCAACGTATGAAACATATAA 243

Qy	3964	gcattaccacacagc	3977
Db	244	GCATTACCCAGAGC	257

RESULT	15
LOCUS	A1365650
DEFINITION	A1365650 490 bp mRNA EST 07-JAN-1999 ap20n08.x1 Schiller oligodendroglioma Homo sapiens cDNA clone IMAGE:1955967 3' similar to TR:Q62179 Q62179 SEMAPHORIN C ; , mRNA

Accession	Length	Organism	Source	Date
A1365650	490 bp	MRNA	EST	07-JAN-1999
ap20h08.x1	Schiller oligodendroglioma	Homo sapiens	CDNA clone	
IMAGE:1955967	3' similar to TR:Q62179	Q62179	SEMAPHORIN C	;', mRNA

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM n cleic - nucleic search, using sw model

Run : June 3, 2000, 01:06:58 ; Search time 5907.01 Seconds
(without alignments)
134.490 Million cell updates/sec

File : US-09-284-180-7

Perfect score: 196
Sequence: 1 aaattgtaccacagctgct.....ggtccaagacatagatcag 196

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Search: 4857316 seqs, 2026611650 residues

Total number of hits satisfying chosen parameters: 9714632

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
18: em_est18:*
19: em_est19:*
20: gb_est1:*
21: gb_est2:*
22: gb_est3:*
23: gb_est4:*
24: gb_est5:*
25: gb_est6:*
26: gb_est7:*
27: gb_est8:*
28: gb_est9:*
29: gb_est10:*
30: gb_est11:*
31: gb_est12:*
32: gb_est13:*
33: gb_est14:*
34: gb_est15:*
35: gb_est16:*
36: gb_est17:*
37: gb_est18:*
38: gb_est19:*
39: gb_est20:*
40: gb_est21:*
41: gb_est22:*
42: gb_est23:*
43: gb_est24:*

44: gb_est25:*
45: gb_est26:*
46: gb_est27:*
47: gb_est28:*
48: gb_est29:*
49: em_est20:*
50: em_est21:*
51: em_est22:*
52: gb_est30:*
53: gb_est31:*
54: gb_est32:*
55: em_est33:*
56: em_est34:*
57: em_est35:*
58: em_est36:*
59: gb_est37:*
60: gb_est38:*
61: gb_est39:*
62: gb_est40:*
63: gb_est41:*
64: gb_est42:*
65: em_est43:*
66: em_est44:*
67: em_est45:*
68: em_est46:*
69: gb_est47:*
70: gb_est48:*
71: gb_est49:*
72: gb_est50:*
73: gb_est51:*
74: gb_est52:*
75: em_est53:*
76: em_est54:*
77: em_est55:*
78: em_est56:*
79: gb_est57:*
80: gb_est58:*
81: gb_est59:*
82: gb_est60:*
83: gb_est61:*
84: gb_est62:*
85: gb_est63:*
86: em_est64:*
87: em_est65:*
88: em_est66:*
89: em_est67:*
90: gb_est68:*
91: gb_est69:*
92: em_est70:*
93: em_est71:*
94: gb_est72:*
95: gb_est73:*
96: gb_est74:*
97: em_est75:*
98: em_est76:*
99: gb_est77:*
100: gb_est78:*
101: em_est79:*
102: em_est80:*
103: em_est81:*
104: em_est82:*
105: gb_est83:*
106: gb_est84:*
107: gb_est85:*
108: gb_est86:*
109: gb_est87:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query	Score	Match	Length	DB	ID	Description
1	196	100.0	503	34	AA459837	AA459837 2x5012.t
2	195	99.5	364	20	T09073	T09073 EST06966 In
3	68	34.7	212	20	242773	242773 HSC0E021 n
4	46	23.5	539	79	AA258432	AA258432 ucq4h08.y
5	45	23.0	357	80	AM345392	AM345392 24958 MAR
6	42.8	21.8	298	60	A1789249	A1789249 a158a10.x
7	41.6	21.2	638	79	AM245910	AM245910 2822888.5
8	40	20.4	639	79	AA245910	AA245910 2822888.5
9	37.6	19.2	750	52	A1651838	A1651838 wds5h11.x
10	37.6	19.2	206	20	T08621	T08621 EST06513 In
11	36.6	18.7	265	20	M78717	M78717 EST00865 H1
12	36.6	18.3	488	81	AA447785	AA447785 89922 MAR
13	35.8	18.3	365	81	AA437778	AA437778 79230 MAR
14	35.6	18.2	487	31	AA285753	AA285753 z552907.t
15	33.4	17.3	737	105	AQ307294	AQ307294 HS-2013_A
16	32	16.3	275	24	H71612	H71612 yu71f07.t
17	32	16.3	365	21	R10186	R10186 yf35d02.t
18	32	16.3	925	82	CNS0091P	A053013 Drosophila
19	31.6	16.1	239	26	M32736	M32736 zc68607.t
20	31.4	16.0	558	29	AA136550	AA136550 z110a06.t
21	31.4	16.0	755	82	AG002305	AG002305 Homo sapi
22	31.2	15.9	301	47	A1615637	A1615637 v124c04.y
23	31.2	15.9	383	47	A1506002	A1506002 v124c04.x
24	31.2	15.9	505	79	AM247066	AM247066 2822608.5
25	31	15.8	506	42	A1122381	A1122381 uc61d09.r
26	30.8	15.7	478	40	AT000144	AT000144 AT000144
27	30.8	15.7	486	24	H63815	H63815 yf52e03.t
28	30.6	15.6	699	106	AAQ25880	AAQ25880 CTRF-El-
29	30.2	15.4	209	34	H72187	H72187 y502b01.t
30	30.2	15.4	480	39	AA866932	AA866932 v042b12.t
31	30	15.3	297	80	AW358571	AW358571 43235 MAR
32	30	15.3	352	24	H70932	H70932 yu70f02.s1
33	29.8	15.2	384	72	AM161457	AM161457 au71b02.y
34	29.8	15.2	399	72	AM161048	AM161048 au71b02.y
35	29.6	15.1	272	69	AM138699	AM138699 UT-H-B11
36	29.6	15.1	281	64	AA068205	AA068205 xeo7b10.x
37	29.6	15.1	535	28	AA068205	AA068205 m94912.t
38	29.4	15.0	466	37	AA736971	AA736971 nw13h05.s
39	29.4	14.9	397	80	AA134885	AA134885 n1438 MAR
40	29.2	14.9	424	26	W94195	W94195 zc77e03.t
41	29.2	14.9	555	52	A1641288	A1641288 fc13a11.y
42	28.2	14.9	564	47	A1473897	A1473897 t168c05.x
43	28.2	14.9	728	41	A1722416	A1722416 fc26n11.x
44	29	14.8	331	45	A1337561	A1337561 q902e02.x
45	29	14.8	388	45	A1377512	A1377512 tc37d11.x

Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel.: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Sed primer: -28ml3 revz ER from Amersham
 High quality sequence stopc: 459.
 Location/Qualifiers
 1..503

```

BASE COUNT      105 a      136 c      149 g      113 t
ORIGIN
/organism="Homo sapiens"
/db_xref="GDB:6039163"
/db_xref="taxon:9606"
/clone="IMAGE:795718"
/clone_1fb="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I -
oligo(dT)
primer [5',
TGTTACCAATCTGACATGGAGCGGCCGCCCAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5 and was
constructed by Bento Soares and M. Fatima Bonaldo."
```

	Query Match	Similarity	100.0%	Score 196:	DB 34:	Length 503:
	Best Local Similarity	100.0%	Pred.	No. 2,6e-49:		
	Matches 196:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:	
Oy	1	aattgtaccacaagcttgcctcccttggttcctccgactcagttgatcacaaagttaataca	60			
Db	175	AAATGTGACCAAGCTGGCTCCTGTTGGTCCCTACTGAGTGACACAAGTGATACCA	234			
Oy	61	aaccaacttggcccgctctccacagatctgtctcagaatgtcatccctggccccagaaccagctcgt	120			
Db	235	ACCAACCTGTGGCCGCTCTCCAGAGCTGCTCAGAGTCATCTCGGCCAAGACCBACTCTGT	294			
Oy	121	gccctggagcttcctccgctcgtgaatgattgttggcccacatgccggaggacacagaggttgttc	180			
Db	295	GCCTGAGACTCTCCGGCTCGATGATGATGTGTGGCCCATCGCGGGAGACACCCAGGGGTTGGTC	354			
Oy	181	caagacataagatcag	196			
Db	355	CAGAATATGAGATCAG	370			

RESULT	2
LOCUS	T09073
DEFINITION	T09073 364 bp mRNA EST T09073 03-Aug-1993 EST06666 Infant Brain, Bento Soares Homo sapiens cdna clone HIBB071 5' end, mRNA sequence.
ACCESSION	T09073
VERSION	T09073.1 GI:390101
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 364)
AUTHORS	Adams,M.D., Soares,M.B., Kerlavage,A.R., Fields,C. and Venter,J.C.
TITLE	Rapid cDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cdna library
JOURNAL	Nature Genet. 4, 373-380 (1993)
MEDLINE	94004965

```

COMM NT      Contact: Adams, MD
              The Institute for Genomic Research
              932 Clopper Road, Gaithersburg, MD 20878
              Tel: 3018699056
              Fax: 3018699423
              Email: mdadams@tigr.org
              Seq primer: M13 Reverse
              Location/Qualifiers
              Source
                1..364
                /organism="Homo sapiens"
                /db_xref="AFCC (Inhost):85555"
                /db_xref="taxon:9606"
                /clone="HIB071"
                /clone_lib="Infant Brain, Bento Soares"

BASE COUNT   70 a 100 c 106 g 85 t 3 others
ORIGIN N

Query Match   99.5%: Score 195; DB 20; Length 364;
Best Local Similarity 99.5%: Pred. No. 4.6e-49;
Matches 195; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 aaattgaccacagctgtgctcctgtgtgctccgctactgaggtgacacagtgataca 60
    |||||||
Db 1 AAATTGTACACAGCTGCTCCTGTGTGCTCCCGTACTGAGGTGACACAGTGAATACA 60
    |||||||

Oy 61 accaaactgtggccgctctccagagctgctcagagtgatcctctggcccaaggaccagtcgt 120
    |||||||
Db 61 ACNACTGTGGCGGCTCTCCAGAGCTCTCAGAGTGCATCTGTGGCCAGCAGACCAAGTCTGT 120
    |||||||

Oy 121 gctctgagcttcctcgctgctgagtggtgtgtgcccacatgctgggagagaccagtggtgtgc 180
    |||||||
Db 121 GCCTGAGCTTCGCGCTGATGATGTGTGTGCCCATGCGGGGAGACCGAGGTTGTGTC 180
    |||||||

Oy 181 caagacatagctcag 196
    |||||||
Db 181 CAAGACATGAGTCAAG 196
    |||||||

RESULT 3
LOCUS       242773      212 bp      mRNA      EST      11-NOV-1994
DEFINITION  HSC07E021 normalized infant brain cDNA Homo sapiens cDNA clone
              c-0le02, mRNA sequence.
ACCESSION   242773
VERSIONS    242773.1 GI:570345
KEYWORDS    EST.
SOURCE      human.
            OR ANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Homiidae; Homo.
            1 (bases 1 to 212)
            Aufferay,C., Behar,G., Bols,F., Bouchard,R., da Silva,C.,
            Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau M.N., Lamy,B.,
            Lorenz,F., Mitchell,H., Mariage-samson,R., Pletu,G., Pouliot,Y.,
            Sebastien-kabackich,C. and Tessier,A.
            IMAGE: molecular integration of the analysis of the human genome
            and its expression
            C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
            95277534
            Contact: Genethon
            Genexpress-Genethon
            Genethon Centre de recherche sur le Genome Humain
            1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
            Tel: 33169472800
            Fax: 33160778698
            Email: genexpress@genethon.fr
            Single read.
            Genexpress_library_id: C; Genexpress_sequence_id: y1c-0le02
            Seq primer: (-21)M13 universal.
            Location/Qualifiers
            1..212
            /organism="Homo sapiens"

FEAT RES
Source

COMM NT      Contact: Adams, MD
              The Institute for Genomic Research
              932 Clopper Road, Gaithersburg, MD 20878
              Tel: 3018699056
              Fax: 3018699423
              Email: mdadams@tigr.org
              Seq primer: M13 Reverse
              Location/Qualifiers
              Source
                1..364
                /organism="Homo sapiens"
                /db_xref="AFCC (Inhost):85555"
                /db_xref="taxon:9606"
                /clone="HIB071"
                /clone_lib="Infant Brain, Bento Soares"

BASE COUNT   70 a 100 c 106 g 85 t 3 others
ORIGIN N

Query Match   99.5%: Score 195; DB 20; Length 364;
Best Local Similarity 99.5%: Pred. No. 4.6e-49;
Matches 195; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 aaattgaccacagctgtgctcctgtgtgctccgctactgaggtgacacagtgataca 60
    |||||||
Db 1 AAATTGTACACAGCTGCTCCTGTGTGCTCCCGTACTGAGGTGACACAGTGAATACA 60
    |||||||

Oy 61 accaaactgtggccgctctccagagctgctcagagtgatcctctggcccaaggaccagtcgt 120
    |||||||
Db 61 ACNACTGTGGCGGCTCTCCAGAGCTCTCAGAGTGCATCTGTGGCCAGCAGACCAAGTCTGT 120
    |||||||

Oy 121 gctctgagcttcctcgctgctgagtggtgtgtgcccacatgctgggagagaccagtggtgtgc 180
    |||||||
Db 121 GCCTGAGCTTCGCGCTGATGATGTGTGTGCCCATGCGGGGAGACCGAGGTTGTGTC 180
    |||||||

Oy 181 caagacatagctcag 196
    |||||||
Db 181 CAAGACATGAGTCAAG 196
    |||||||

RESULT 4
LOCUS       AM258432      539 bp      mRNA      EST      23-DEC-1999
DEFINITION  uc34h08.y1 NCI CGAP Mam5 mus musculus cDNA clone IMAGE: 5' similar
              to TR:064151 Q64151 SEMAPHORIN I ;, mRNA sequence.
ACCESSION   AM258432
VERSION     AM258432.1 GI:6631413
KEYWORDS    EST.
SOURCE      house mouse.
            ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 539)
            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
            On May 18, 1998 this sequence version replaced gi:3137576.
            Other ESTs: uc34h08.x1
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert.Strausberg@nih.gov
            Tissue procurement: Lothar Hennighausen Ph.D., Robin Humphreys
            cDNA library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
            DNA sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNLN at:
            www-bio.lnl.gov/dbtrp/image/image.html

FEAT RES
Source

Seq primer: -40RP from Glbco
High quality sequence stop: 412.
Location/Qualifiers
1..539
/organism="Mus musculus"
/strain="C57/B6"
/db_xref="taxon:10090"
/clone="IMAGE:"
/clone_lib="NCI CGAP Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"

```

/note="Organ: mammary; Vector: pcMV-SPORT6; Site_1: Salt; Site_2: Notti; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lohar Hennighausen/Robin Humphreys, NIH"

BASE COUNT 106 a 157 c 141 g 135 t

Query Match 23.5%; Score 46; DB 79; Length 539;
Best Local Similarity 54.0%; Pred. No. 0.00056;
Matches 94; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

18 gctccgtggtggtccgctgactgaggtgacacagtgatcaacacacgtggtccgtct 77
|||||
32 gctcttgcctggtggtccgctgactggtggtggtggtggtggtggtggtggtggt 91
|||||
78 ccagagctggtcagagtgatcctggtggtggtggtggtggtggtggtggtggtggt 137
|||||
92 ccgttctgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 151
|||||
138 ggtgagtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 191
|||||
152 cagcgcgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 205
|||||

RESULT 5
AM345392 257 bp mRNA EST 01-FEB-2000
LOCUS
DEFINITION 24958 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION AM345392
VERSION AM345392.1 GI:6843102
KEYWORDS
SOURCE
ORGANISM Bos taurus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 257)
Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A. and Keeler,J.W.
Design and use of four pooled tissue normalized cDNA libraries for EST discovery in cattle
Unpublished (2000)
On Jun 22, 1998 this sequence version replaced gi:3246885.
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithem@mail.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -mismatch 12 options.

PCR Primers
FORWARD: AGCAACACGATGACCAT
BACKWARD: GTTCCAGTCACGACG
Plate: 13 row: 1 column: 1
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
1. 257

FEATURES

source

1. 257

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="MARC 4BOV"

/tissue_type="pooled"

/lab_host="DH10B"

/note="Vector: pcMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 20 and day 40 embryos."

BASE COUNT 50 a 80 c 82 g 45 t

ORIGIN

92 a 104 c 118 g 83 t 1 others

Query Match 23.0%; Score 45; DB 80; Length 257;
Best Local Similarity 67.7%; Pred. No. 0.00085;
Matches 63; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

62 ccactgtggtccgtcctcagagctgctcagagtgatcctggtggtggtggtggtggt 121
|||||
6 CCACCTGACGCTGTACACAGCTGCGAGGAGCCTGCTGCGCCGAGGACCTACTATCG 65
|||||

122 cctgagcttcggtggtggtggtggtggtggtggtggtggtggtggtggtggt 154
|||||
66 CTGAGACGCTGAGGAGCTGCTGCGCTGAGCC 98
|||||

RESULT 6
A1787249 398 bp mRNA EST 02-JUL-1999
LOCUS
DEFINITION u158a10.x1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1924122 3' similar to TR:062179 062179 SEMAPHORIN C, mRNA sequence.
A1787249
VERSION A1787249.1 GI:5334965
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 398)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohr,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
On Dec 20, 1995 this sequence version replaced gi:1131162.
Other ESTs: u158a10.y1
Contact: Maria M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:980414
Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 289.
Location/Qualifiers
1. 398

FEATURES
source
1. 398
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone_image="1924122"
/clone_lib="Sugano mouse liver mlia"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: liver; Vector: pME18S-FLJ; Site_1: DraIII (CACTGTG); Site_2: DraIII (CACCATGT); 1st strand cDNA was primed with an oligo(dT) primer [ATGCGCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTGCGCTACTGCG], digested and cloned into distinct DraIII sites of the pME18S-FLJ vector (5' site CACTGTG, 3' site CACCATGT). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTGCTCTTAAAGTGGC and 3' end primer CGACCTGCGCTGAGACACA."

BASE COUNT

92 a 104 c 118 g 83 t 1 others

QY 18 gctcttggtggtccctccgtactgagtgacacaaagtacacaaactgtgcccgtct 77
 DB 542 GCTCTTGCCGGCTCCCGCTCCAGCTGCTGACCTGCGCCGTGCATTAAGTA 483
 QY 78 ccagagctgctcagagtgatcctctgcccagaccagctctgtctcctggagcttcggct 137
 DB 482 TCGCTCTGTGCAAGACTGTCTGCTGCGCCGGGACCCCTATTGCGCTGACGTCACAC 423
 QY 138 ggaatgagtggtggccatgcgg 161
 DB 422 CAGCCGCTGTGTGGCCGTGGGTGG 399

RESULT 9
 A1638881 710 bp mRNA EST 14-DEC-1999
 LOCUS t080d08.x1 NCI-CGAP-GC6 Homo sapiens cDNA clone IMAGE:2240175 3'
 DEFINITION similar to TR:064151 064151 SEMAPHORIN I, mRNA sequence.
 ACCESSION A1638881
 VERSION A1638881.1 GI:4691115
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 710)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT On Mar 10, 1998 this sequence version replaced gi:2948370.
 CONTACT: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

JOURNAL
 COMMENT
 Insert Length: 793 Std Error: 0.00
 Seq primer: -40bp from Gibco
 High quality sequence stop: 444.
 Location/Qualifiers
 1..710
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2240175"
 /clone_id="NCI-CGAP GC6"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH108"
 /note="vector: p7733-Pac (Pharmacia) with a modified
 polylinker. Plasmid DNA from the normalized library
 NCI-CGAP-GC4 was prepared, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from a pool of 5,000 clones made
 from the same library (clones 1257096-1258631,
 1469064-1470963, and 1475592-1476743). Subtraction by
 Bento Soares and M. Fatima Bonaldo."

BASE COUNT 171 a 190 c 183 g 165 t 1 others
 ORIGIN

Query Match 20.4%; Score 40; DB 52; Length 710;
 Best Local Similarity 54.9%; Pred. No. 0.04;
 Matches 79; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 18 gctcttggtggtccctccgtactgagtgacacaaagtacacaaactgtgcccgtct 77
 DB 543 GCTCTTGCCGGCTCCCGCTCCAGCTGCTGACCTGCGCCGTGCATTAAGTA 484
 QY 78 ccagagctgctcagagtgatcctctgcccagaccagctctgtctcctggagcttcggct 137
 DB 483 TCGCTCTGTGCAAGACTGTCTGCTGCGCCGGGACCCCTATTGCGCTGACGTCACAC 424
 QY 138 ggaatgagtggtggccatgcgg 161
 DB 423 CAGCCGCTGTGTGGCCGTGGGTGG 400

RESULT 10
 T08621 206 bp mRNA EST 03-AUG-1993
 LOCUS EST06513 Infant Brain, Bento Soares Homo sapiens cDNA clone H1BBH20
 DEFINITION 5' end, mRNA sequence.
 ACCESSION T08621
 VERSION T08621.1 GI:389649
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 206)
 AUTHORS Adams,M.D., Soares,M.B., Kerlavage,A.R., Fields,C. and Venter,J.C.
 TITLES Rapid cDNA sequencing (expressed sequence tags) from a
 directionally cloned human infant brain cDNA library
 JOURNAL Nature Genet. 4, 373-380 (1993)
 MEDLINE 94004965
 COMMENT Contact: Adams, MD
 The Institute for Genomic Research
 932 Clapper Road, Gaithersburg, MD 20878
 Tel: 3018699056
 Fax: 3018699423
 Email: mdadams@tigr.org
 Seq primer: M13 Reverse.

FEATURES
 source 1..206
 /organism="Homo sapiens"
 /db_xref="ATCC (inhost):95136"
 /db_xref="taxon:9606"
 /clone="H1BBH20"
 /clone_id="Infant Brain, Bento Soares"

BASE COUNT 30 a 66 c 56 g 50 t 4 others
 ORIGIN

Query Match 19.2%; Score 37.6; DB 20; Length 206;
 Best Local Similarity 52.8%; Pred. No. 0.13;
 Matches 76; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
 QY 18 gctcttggtggtccctccgtactgagtgacacaaagtacacaaactgtgcccgtct 77
 DB 6 GCTCTTGCCGGCTCCCGCTCCAGCTGCTGACCTGCGCCGTGCATTAAGTA 65
 QY 78 ccagagctgctcagagtgatcctctgcccagaccagctctgtctcctggagcttcggct 137
 DB 66 TCGCTCTGTGCAAGACTGTCTGCTGCGCCGGGACCCCTATTGCGCTGACGTCACAC 125
 QY 138 ggaatgagtggtggccatgcgg 161
 DB 126 CAGCCGCTGTGTGGCCGTGGGTGG 149

RESULT 11
 M78717 265 bp mRNA EST 26-MAY-1992
 LOCUS EST00865 Hippocampus, Striatogene (cat. #36205) Homo sapiens cDNA.
 DEFINITION clone HHCMD08, mRNA sequence.
 ACCESSION M78717
 VERSION M78717.1 GI:273032

[illegible]

FEATURES	Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options.			
SOURCE	PCR Primers FORWARD: AGGAACAGCTATGACCAT BACKWARD: GTTTCACGTCACGACG Plate: 76 row: L column: 1 Seq primer: ATTAGAGACACTATAG.			
Location/Qualifiers	1..488 /organism="Bos taurus" /db_xref="taxon:9913" /clone_id="MARC 1BOY" /tissue_type="pooled" /lab_host="DH108" /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."			
BASE COUNT	65 a	187 c	142 g	94 t
ORIGIN				
Query Match	18.7%	Score 36.6;	DB 81;	Length 488;
Best Local Similarity	55.0%	Pred. No. 0.37;		
Matches	72;	Conservative	0;	Mismatches 59; Indels 0; Gaps 0;
Oy	24	ggttgctcccgctactggtggtgacacaaagtgaatacacaacactgtggcgcgtccagag 83		
Db	1	GGCGGTTCCAACTCAGCGCGGTGTCAGAGCCCTCTTGCCCTTCTCGGGAAGCAAGCGAC 60		
Oy	84	ctgtctcagaagtgcattcctgtgcccagagaccagctctgtgctctgagcttcgcgctgatatga 143		
Db	61	CTGCAGAGACGTGCGGTCTTCCGCGGAGACCCTACTGCGCTGTGAGCCCGCGCGTGGCGCG 120		
Oy	144	gtgtgtgtggccc 154		
Db	121	CTGTGTGCGCC 131		
RESULT	13			
LOCUS	AM437778	365 bp	mRNA	EST
DEFINITION	79230 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.			14-FEB-2000
ACCESSION	AM437778			
VERSION	AM437778.1			GI:6973084
KEYWORDS	EST.			
SOURCE	Bos taurus.			
ORGANISM	Bos taurus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; Bovidae; Bovinae; Bos. 1 (bases 1 to 365) Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A. and Keefe,J.W. Design and use of four pooled tissue normalized cDNA libraries for EST discovery in cattle Unpublished (2000) On Jan 6, 2000 this sequence version replaced gi:6675875. Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smtlhemal.marc.usda.gov Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options.			
TITLE	PCR Primers			
JOURNAL	FORWARD: AGGAACAGCTATGACCAT BACKWARD: GTTTCACGTCACGACG Plate: 39 row: M column: 15			
COMMENT	Seq primer: ATTAGGTGACACTATAG.			

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FEAT1 RES      Location/Qualifiers
SOURCE          1.365
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                /db_xref="taxon:9913"
                /clone_11b="MARC 1B0V"
                /tissue_type="pooled"
                /lab_host="DH10B"
                /note="Vector: pcMV SPOR6; Site_1: XbaI; Site_2: XhoI;
                library made from pooled tissue from lymph node, ovary,
                fat, hypothalamus, and pituitary."
BASE COUNT     49 a 138 c 104 g 74 t
ORIGIN
Que cy Match    18.3%; Score 35.8; DB 81; Length 365;
Bsc Local Similarity 55.1%; Pred. No. 0.58;
Matches 70; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
OY 28 ggtccgactgaggtgacacaagtgatgatacacaacgaactgtgscgtctccagagctgc 87
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 56 ggttcCAACTCAGCGGTGATGCAGGCCCTTCGTGGCTTCTGCGGAGACGATGCACCTGC 115
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 88 tcagatgacatccctgagccagagccagctgctgtccgtgaggttcgcgtgataagagct 147
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 116 GAGGAGCTGGTCTCTTCGCCGAGACCCCTTACTGCGCTGTGAGGCCCGGCCCTGCGCCCTCT 175
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 148 gtgagcc 154
    || ||||
DB 176 GTCGCC 182
RESUI F 14
AA287573
LOCUS          AA287573
DEFINITION    AA287573.1 NC1_CGAP.GCB1 Homo sapiens cDNA clone IMAGE:701148 5'
ACCESSION     AA287573
VERSION       AA287573.1 GI:1933255
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 487)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1288732.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 486-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 474.
Location/Qualifiers
1.487
/organism="Homo sapiens"
/db_xref="GDB:5740583"
/db_xref="taxon:9606"
/clone_11b="NC1_CGAP.GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/note="Vector: p7773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - Oligo(dT) primer
[5'-GTGTACCAATCTGAAGTGGAGCGGCCCTCATTTTTTTTTTTTTT-

```

[illegible]

	Matches	74:	Conservative	0:	Mismatches	46:	Indels	3:	Gaps	1:
Oy	32	ccccctactgaggtgacacaagtgaatacaaacacactgtg--gcgctctccagagctgct	88							
Db	691	CCCATGTTAAGGTGAGACAATTAATTCAAAGAACAATGTTTCCGCTGCAAGGCATT	632							
Oy	89	cagagtcgcatcctgagccagctcgtgctgagagctccggctgagatgagtgtg	148							
Db	631	CAGGCTGTGGCCTGGCCCAAAACCATTTCTTTATATAGCTTATGGCCCTGTGATGAG	572							
Oy	149	tgg 151								
Db	571	GGC 569								

Search completed: June 3, 2000, 01:07:02
 Job time: 58233 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM n cleic - nucleic search, using sw model

Run n : June 3, 2000, 01:06:50 ; Search time 5907.01 Seconds
(Without alignments)
1208.348 Million cell updates/sec

Title : US-09-284-180-5

Perf ct score : 1761
Sequence : 1 ggggggtgcctctatgctgc.....catgtgatgaacatccatc 1761

Scoring table : IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched : 4857316 seqs, 2026611650 residues

Total number of hits satisfying chosen parameters : 9714632

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_est1:*
2: em_est2:*
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108: gp_est62:*
109: gp_est63:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NC	Score	Query Match	Length	DB	ID	Description
1	476.4	27.1	503	34	AA459837	AA459837 zx50g12.r
2	356.2	20.2	364	20	T09073	T09073 EST06966 in
3	349.2	19.8	517	22	R54387	R54387 y878f12.r1
4	338.4	19.0	337	20	Z45339	Z45339 HSC2M091.n
5	328.4	18.6	437	23	H24181	H24181 ym5f02.r1
6	326.4	18.5	347	22	H10623	H10623 ym08f07.r1
7	308.2	17.5	376	81	AM436751	AM436751 77209.MAR
8	229.4	13.0	592	106	AQ352219	AQ352219 CTBI-EI-
9	167	9.5	208	81	AM436702	AM436702 77141.MAR
10	141	8.0	212	20	Z42773	Z42773 HSC0E021.n
11	112.6	6.4	232	80	AM346693	AM346693 29273.MAR
12	112.6	6.4	232	80	AM346698	AM346698 29282.MAR
13	98.4	5.6	430	45	AI365650	AI365650 ap20h08.x
14	93.2	5.3	619	64	AL118624	AL118624 DKF2P61F
15	84.6	4.8	442	48	AI555178	AI555178 UT-R-C2P
16	76.2	4.3	638	79	AM245910	AM245910 2822888.5
17	72.4	4.1	942	69	AM078986	AM078986 A0078986
18	67.8	3.9	462	42	AI141990	AI141990 ooi17910.x
19	67.4	3.8	555	52	AI641288	AI641288 fc13a11.y
20	57.8	3.3	925	82	CNS0091P	AL053013 Drosophila
21	55.6	3.2	398	60	AI787249	AI787249 u58a10.x
22	50	2.8	203	31	AA326134	AA326134 EST29247
23	46.8	2.7	539	79	AM258432	AM258432 ug34h08.y
24	46.6	2.6	492	27	AA023538	AA023538 mh75d07.r
25	45.8	2.6	498	29	AA190645	AA190645 zq44a06.r
26	45	2.6	257	80	AM345392	AM345392 24958.MAR
27	44	2.5	900	54	C82295	C82295 C82295 Leuk
28	43.6	2.5	320	74	AM227926	AM227926 up19b05.y
29	43.6	2.5	889	74	AU050267	AU050267 AU050267
30	43.4	2.5	624	74	AM328571	AM328571 d803d12.x
31	42.6	2.4	997	82	CNS006DN	AL065132 Drosophila
32	42.6	2.4	1049	83	CNS015B1	AL105223 Drosophila
33	41.8	2.4	266	20	Z28925	Z28925 HSC1H081.S
34	41.8	2.4	839	82	CNS004NB	AL054280 Drosophila
35	41.6	2.4	733	82	CNS011AC	AL100014 Drosophila
36	41.4	2.4	608	44	AI258757	AI258757 LP02029.5
37	40.8	2.3	478	24	H73136	H73136 yu03f07.r1
38	40.2	2.3	1101	83	CNS017SY	AL108460 Drosophila
39	40	2.3	659	52	AI651838	AI651838 wb55h11.x
40	40	2.3	710	52	AI638881	AI638881 t08d08.x
41	39.8	2.3	479	81	AM438208	AM438208 707067D05
42	39.8	2.3	486	23	H20378	H20378 yu61d07.r1
43	39.8	2.3	641	81	AM433361	AM433361 707067D05
44	39.2	2.2	409	23	D52750	D52750 HUM086G12B
45	39.2	2.2	964	82	CNS003WG	AL065254 Drosophila

ALIGNMENTS

Result LOCUS	AA459837	503 bp	mRNA	EST	09-JUN-1997
DEFINITION	zx50g12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795718				
ACCESSION	AA459837				
VERSION	AA459837.1				
KEYWORDS	EST				
SOURCE	human				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
REFERENCE	Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
REFERENCE	1 (bases 1 to 503)				
REFERENCE	Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,				
REFERENCE	Kucaba, T., Lacey, M., Le, N., Lennon, G., Marra, M., Martin, J.,				
REFERENCE	Moore, B., Schellenberg, K., Steptoe, W., Tan, F., Theising, B.,				
REFERENCE	White, Y., Wylie, T., Waterston, R., and Wilson, R.				
REFERENCE	WashU-Merck EST Project 1997				
REFERENCE	Unpublished (1997)				
REFERENCE	On Sep 12, 1996 this sequence version replaced gi:1392936.				

Query Match	27.1%	Score 476.4	DB 34	Length 503
Best Local Similarity	99.4%	Pred. No. 1.3e-117		
Matches 499	Conservative 0	Mismatches 1	Indels 2	Gaps 2
748	gacctctcagaagtcggtgcccacaggtgacacagctcctcagaagaaagatgatg	807		
1	GCCTCTCAGAGTGTGTGCCCACCA-GGTGACACACCTCTCAGGAAAGATGATGTG	59		
808	cctcaccgggggaca-gagagtgagacacccacacagacagtcgagtcgagtc	866		
60	CTCTACCTGGGACATGAGATGACACCTCCACGACAGTGGATCGAGTCACACT	119		
867	cagcgtctctgagaatctgagccttattccacagacacagcagtcgagtcgagtc	926		
120	CAGCGTCTTGAGATCTGCGCTTATCCAGACACACAGTGTGAGACATGAAAT	179		
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180	GTACACACAGCTGCTCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	239		
987	ctgtgcccgtctcagaagtcctcagagtcgagtcgagtcgagtcgagtcgagtc	1046		
240	CTGTGCGGCTCTCCAGACTGCTAGAGTGCATCTGCGCCACAGACAGTGTGCTG	299		
1047	gagcttcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtc	1106		
300	GAGCTTCCGCGCTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	359		
1107	catagagtcagcagatgctctctcttctgtctcctaaagagtcgagtcgagtc	1166		
360	CATAGAGTCAGCAGATGCTCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	419		
1167	gtttaaagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtc	1226		
420	GTTTAAATTCCTCCGCTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	479		
1227	atggcagtcagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtc	1248		
480	ATGGCAGTCAGTCGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	501		

Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 459.

FEATURES

source
1..503
/organism="Homo sapiens"
/db_xref="GDB:6039163"
/db_xref="taxon:9606"
/clone="IMAGE:795718"
/clone_id="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73D vector. Library
went through one round of normalization to Colb, and was
constructed by Benito Soares and M. Fatima Bonaldo."

RESU_T	2
LOCUS	T09073 364 bp mRNA EST 03-AUG-1993
DEFINITION	E8T06966 Infant Brain, Bento Soares Homo sapiens CDNA clone HIBO7.
ACCESSION	5' end, mRNA sequence. T09073 T09073.1 GI:390101
VERSIONS ON KEYWORDS	EST. human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Euarchonta; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 364) Adams,M.D., Soares,M.B., Karlavag,A.R., Fields,C. and Venter,J.C. Rapid CDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library Nature Genet. 4, 373-380 (1993)
JOURNAL	94004965
COMMENTARY	Contact: Adams, MD The Institute for Genomic Research 932 Clopper Road, Gaithersburg, MD 20878 Tel.: 3018699056 Fax: 3018699423 Email: mdadams@ligr.org Seq primer: M13 Reverse.
FEATURE SOURCE	Location/Qualifiers 1..364 /organelle="Homo sapiens" /db_xref="ATCC (InHost):85555" /db_xref="taxon:9606" /codon="HIBO71" /cloned_lib="Infant Brain, Bento Soares"
BASE COUNT	70 A 100 C 106 G 85 T 3 others
ORIGIN	
Quality Match	20.2%; Score 356.2; DB 20; Length 364;
Beit Local Similarity	98.4%; Pred.No. 2,3e-85;
Matches 358; Conservative	0; Mismatches 6; Indels 0; Gaps 0.
OY	922 aaatgtaccacgacggcttgccttggttttcctcccgactcgaaggtagtacaaagttaaca 981
Dd	1 AAATTGTACCAGACTGCTCCTGGTGCTGCCGTAAGTAGGTGCACAAGAATAACA 60
OY	982 accaacctgtgcgcgtctcacagaagctcatagaattgatctcgtgcccaaggaccacgactgt 1041
Dd	61 ACNAACTGGCGCGTCCTCCAGAGCTGCTCAGAGTGATCATCTGGCCCCAAGCAAGCTGTG 120
OY	1042 gcccttgagcttcctcgcgtcttgatagtgtgtgtgtcccattgcggggaggaccagaggttgttc 1101
Dd	121 GCCTGAGAGTTCCCGCTGGATGAGTGTGGCCCATGCGGGGAGCACCGAGGGTTGGTC 180
OY	1102 caaagcataagatcagacgaatgtctcctcttctgtgtcctaagaagacctgagaagatcca 1161
Dd	181 CAAGCATATGAATCAACAGATGTCTCTTTGTGTGTCTTAAGAGCTTGAGAACATCCA 240
OY	1162 gtagtgtttaaatgtccgtgtgctacagctgtgcgacatgtgtcttgcacatgtttcccaagc 1221
Dd	241 GTAGGTGTGAAGTTCCTCCGTGGCTACAGNTGGCATGTGGTCTTNCCATGTTCTCCAAAG 300
OY	1222 tcagatatgggcatcctcgtgtgtgtgacacggccccagtgaggtgtagtatccatcccccggg 1281
Dd	301 TCAGCATGGGCATCCTGTGTGTGGCACCAAGCCAGTGGAGTACTTACCCCCTGG 360
OY	1282 ccgg 1285
Dd	361 CGGG 364

LOCUS	517 bp	mRNA	EST	18-MAY-1995
DEFINITION	R548f12.r1 Soares infant brain INIB Homo sapiens CDNA clone IMAGE:39491.5'	similar to SP:A49069 A49069 COLLABSIN - , mRNA sequence.		
ACCESSION	R54387			
VERSION	R54387.1	GI:816289		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukariota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
AUTHORS	1 (bases 1 to 517) Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.			
TITLE	The Mashu-Merck EST Project			
JOURNAL	Unpublished (1995)			
COMMENT	Contact: Wilson RK Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: east@watson.wustl.edu Insert Size: 2134 High quality sequence stops: 99 Source: IMAGE Consortium, LNL. This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Insert Length: 2134 Std Error: 0.00 Seq primer: M13RPI High quality sequence stop: 99. Location/Qualifiers 1..517 /organism="Homo sapiens" /db_xref="GDB:412032" /db_xref="taxon:9606" /clone IMAGE:39491" /clone_lib="Soares infant brain INIB" /sex="female" /dev_stage="73 days post natal" /lab_host="DB10B (ampicillin resistant)" /note="Organ: whole brain; Vector: Lnfmd BA; Site:1: Not I; Site:2: Hind III; 1st strand cDNA was primed with a Not I - Oligo(dT) primer [5' AACGAGAAGATTGCGCGCCGACAGAAATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lnfmd BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."			
FEATURES				
source				
BASE COUNT	123 a 137 c 128 g 118 t			
ORIGIN				
Query Match	19.8%	Score 349.2;	DB 22;	Length 517;
Best Local Similarity	95.1%	Pred. No. 2.1e-83;		
Matches 411; Conservative	0;	Mismatches 14;	Indels 7;	Gaps 5;
488	gaccacaagaacatcgcgcagcagtcgtaatggtccctcagagaactaaacatgactgca	547		
Db	1 GACCACAGACATTCGGACAGTCGTGATGTCCTTCAGAGAACTAAACATGACTGCA	60		
Qy	acagagagcctgctgctgtgacaaatgatgtgccccagaccagacctggagatgcatca	607		
Db	61 ACAGAGGAGCTGCTGCTGTCGACATGATGTGTCGCCACCCAGACCTTGAGAGTGCATCA	120		
Qy	ccaacaacataaagctcgcgcgacattgctcatctctccctgccttcagcgcgaacca	667		
Db	121 CCAACAACATGAAGCTCCGGCATTGGCTATCTCTCTCCCTGCTTACCGCGACTCA	180		
Qy	ccctcatccggagaccaccacatcatgagcagcagtgcttcacagtatgagccacccc	727		

Db 181 CCTCATCCGGAGACACCACCATCATGACAGCCAGTTTTCACGCTGATGCCACCC 240

Qy 728 TCTGTCACCTACAGATACAGATACCTACAGATCGTGGCCAGAGGTCAGCAGCTCT 787

Db 241 TGNMGTCACACAGATACAGATACCTACAGATCGTGGCCAGAGGTCAGCAGCTCT 300

Qy 788 CAGGGAAGAGTATGATGCTCTACCTCGGGGACAGAGGATGGACACTTCACCGAGC 845

Db 301 CAGGGAAGAGTATGATGCTCTACCTCGGGGACAGAGGATGGACACTTCACCGAGC 360

Qy 846 AGTCGAGGATCGAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTC 900

Db 361 AGTCGAGGATCGAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTC 420

Qy 901 CCACAGCAGCT 912

Db 421 TCACAGCAGCT 432

RESULT 4

LOCUS 245329 337 bp mRNA EST 14-NOV-1994

DEFINITION HSC2MG091 normalized infant brain CDNA Homo sapiens CDNA clone

ACCESSION 245329, mRNA sequence.

VERSION 245329.1 GI:574541

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 337)

AufRAY, C., Behar, G., Bols, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houllgate, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pletu, G., Pouillot, Y., Sebastien-Kabatchis, C. and Tessier, A.

IMAGE: molecular integration of the analysis of the human genome and its expression

C.R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)

JOURNAL 95277534

MEI JINE

COMMENT Contact: Genethon

Genethon

Genethon Centre de recherche sur le Genome Humain

1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE

Tel: 33169472800

Fax: 33160778698

Email: genexpress@genethon.fr

Single read.

Genexpress library Idt: C. Genexpress_sequence_idt: y1c-2mg09

Seq primer: (-21)M13_universal.

FEATURES

Source

1. 337

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="c-2mg09"

/clone_lib="normalized infant brain CDNA"

/sex="Female"

/tissue_type="total brain"

/dev_stage="3 months old"

/note="Organ: brain; Vector: lafmid BA; Site:1: HindIII; Site:2: NotI; sex:Female; dev:stage:3 months old; isolate-muscular atrophy patient; tissue_type:total brain; total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector. Clone library from B.Souares, Psychiatry Dept. Columbia University, USA. Normalization_method: Bento Soares, P.N.A.S in press"

BASE COUNT 81 a 106 c 82 g 67 t 1 others

ORIGIN

Quey Match 19.0% Score 334.4; DB 20; Length 337;

Best Local Similarity 99.4% Pred. No. 1.6e-79;

Matches 335; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 487 CGACCAAGACATTCGAGACAGTCTGATGCTCCTTCAGAGAACTAAGATGCTG 546

Db 1 CGACCAAGACATTCGAGACAGTCTGATGCTCCTTCAGAGAACTAAGATGCTG 60

Qy 547 AAGCAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 606

Db 61 AAGCAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120

Qy 607 ACCAACAATGAAGCTCCGACCTTGGCTCATCTCTCCCTGCTGACCGCTGCTC 666

Db 121 ACCAACAATGAAGCTCCGACCTTGGCTCATCTCTCCCTGCTGACCGCTGCTC 180

Qy 667 ACCTTCCGAGGACCACTGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 726

Db 181 ACCTTCCGAGGACCACTGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240

Qy 727 CTGCTGCTACCTAGATGATGATGATGATGATGATGATGATGATGATGATGATG 786

Db 241 CTGCTGCTACCTAGATGATGATGATGATGATGATGATGATGATGATGATGATG 300

Qy 787 TCAAGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 823

Db 301 TCAAGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 337

RESULT 5

LOCUS H24181 437 bp mRNA EST 06-JUL-1995

DEFINITION ym5f02_r1 Soares infant brain INTB Homo sapiens CDNA clone

IMAGE:52280 5' similar to SP:A49065 A49065 COLLAPSE - ;, mRNA sequence.

ACCESSION H24181 GI:892876

VERSION H24181.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 437)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.wustl.edu

Insert Size: 1989

High quality sequence stops: 310 Source: IMAGE Consortium, LINT

This clone is available royalty-free through LINT; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1989 Std Error: 0.00

Seq primer: M13Rpi

High quality sequence stop: 310.

FEATURES

Source

1. 437

/organism="Homo sapiens"

/db_xref="taxon:9606"

/db_xref="taxon:9606"

/clone_lib="IMAGE:52280"

/clone_lib="Soares infant brain INTB"

/sex="Female"

/dev_stage="73 days post natal"

/lab_host="DH10B (ampicillin resistant)"

/note="Organ: whole brain; Vector: lafmid BA; Site:1: NotI; Site:2: Hind III; 1st strand CDNA was primed with a Not

I - oligo(dT) primer [5';
 ACTGAGAGATTTCGGCCGACAGATTTTCTTTTCTTTT 3'];
 double-stranded cDNA was ligated to Hind III adaptors
 (Pharmacia), digested with Not I and directionally cloned
 into the Not I and Hind III sites of the Lactid BA vector.
 Library went through one round of normalization. Library
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 105 a 122 c 112 g 95 t 3 others

Query Match 18.6%; Score 328.4; DB 23; Length 437;
 Best Local Similarity 97.5%; Pred. No. 7.4e-78;
 Matches 344; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

OY 488 gaccacaagacatctgcagcagtcgtaagtgtcccttcagagaactaaacatgactga 547
 |||||||
 DB 1 GACCCAGAGACTTTCGACAGCTGATGCTCCTTCAGAGACTAAACATGACTGCA 60
 |||||||

OY 548 acagagagactgcctgtcgtgacaatgagtgtcccaagccagacctggagagtcacaa 607
 |||||||
 DB 61 ACAGAGGACTGCTGTCTGTGAGCAATGATGTGCCCCAGGCCAGACCTGGAGAGTGCATCA 120
 |||||||

OY 608 ccaacaacatgaagctcgcagccttgcctcctcctcctcctcctcctcctcctcctcctc 667
 |||||||
 DB 121 CCACACATATGAGCTTCGGGACCTTGGCTCATCTCTCTCCTGCTGACCGGATCTCA 180
 |||||||

OY 668 ccttcacccggagac 727
 |||||||
 DB 181 CCTTATCCGGGACACCCACATGAGAGCCAGTGTTCACCTGATGAGCCACCC 240
 |||||||

OY 728 tctgtgtactacacagatacagcctatctcagagctgtgagccagaggtgacagcctct 787
 |||||||
 DB 241 TGCTGTACTACATACATACAGCTATCTCAGAGTGTGCCCCACAGAGGAGACACCTTT 300
 |||||||

OY 788 cagggaaagatgatgtgtctct--acctggagacagagatgacacctcc 838
 |||||||
 DB 301 TAGGGAAGAGATGATGATGTCTTACTCTGGGGACAGAGATGAGACACTTTC 353
 |||||||

RESULT 6
 H10623 347 bp mRNA EST 23-JUN-1995
 LOCUS ym8907.r1 Soares Infant Brain INIB Homo sapiens cDNA clone
 DEFINITION IMAGE:47298 5' similar to SP:A49069 A49069 COLLABSIN - ; mRNA
 sequence.

ACCESSION H10623
 VERSION H10623.1 GI:875445
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 347)
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
 Paterson, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
 Tevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
 Wilson, R.
 The WashU-Merck EST Project
 Unpublished (1995)
 On May 10, 1995 this sequence version replaced gi:805665.
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 Insert Size: 1985
 High quality sequence stops: 198
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.

Insert Length: 1985 Std Error: 0.00
 Seq Primer: M13RPI
 High quality sequence stop: 198.
 Location/Qualifiers
 1. 347
 /organism="Homo sapiens"
 /db_xref="GDB:419839"
 /db_xref="taxon:9606"
 /clone="IMAGE:47298"
 /clone_id="Soares Infant Brain INIB"
 /sex="female"
 /dev_stage="73 days post natal"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: whole brain; Vector: Lactid BA; Site: 1: Not
 I; Site 2: Hind III; 1st strand cDNA was primed with a Not
 I - oligo(dT) primer [5';
 ACTGAGAGATTTCGGCCGACAGATTTTCTTTTCTTTT 3'];
 double-stranded cDNA was ligated to Hind III adaptors
 (Pharmacia), digested with Not I and directionally cloned
 into the Not I and Hind III sites of the Lactid BA vector.
 Library went through one round of normalization. Library
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 82 a 105 c 87 g 67 t 6 others

Query Match 18.5%; Score 326.4; DB 22; Length 347;
 Best Local Similarity 98.5%; Pred. No. 2.3e-77;
 Matches 327; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 488 gaccacaagacatctgcagcagtcgtaagtgtcccttcagagaactaaacatgactga 547
 |||||||
 DB 1 GACCCAGAGACTTTCGACAGCTGATGCTCCTTCAGAGACTAAACATGACTGCA 60
 |||||||

OY 548 acagagagactgcctgtcgtgacaatgagtgtcccaagccagacacacacacacacacacac 607
 |||||||
 DB 61 ACAGAGGACTGCTGTCTGTGAGCAATGATGTGCCCCAGGCCAGACCTGGAGAGTGCATCA 120
 |||||||

OY 608 ccaacaacatgaagctcgcagccttgcctcctcctcctcctcctcctcctcctcctcctc 667
 |||||||
 DB 121 CCACACATATGAGCTTCGGGACCTTGGCTCATCTCTCCTGCTGACCGGATCTCA 180
 |||||||

OY 668 ccttcacccggagac 727
 |||||||
 DB 181 CCTTATCCGGGACACCCACATGAGAGCCAGTGTTCACCTGATGAGCCACCC 240
 |||||||

OY 728 tctgtgtactacacagatacagcctatctcagagctgtgagccagaggtgacagcctct 787
 |||||||
 DB 241 TGCTGTACTACATACATACAGCTATCTCAGAGTGTGCCCCACAGAGGATGAGACACTT 300
 |||||||

OY 788 cagggaaagatgatgtgtctctcctcctcctcctcctcctcctcctcctcctcctcctc 819
 |||||||
 DB 301 CAGGGAAGAGATGATGATGTCTTACTCTGGGGACAGAGATGAGACACTTTC 352
 |||||||

RESULT 7
 AM436751 376 bp mRNA EST 14-FEB-2000
 LOCUS 77209 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
 DEFINITION AM436751
 ACCESSION AM436751
 VERSION AM436751.1 GI:6972057
 KEYWORDS EST.
 SOURCE Sus scrofa
 pig.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 1 (bases 1 to 376)
 Fahnenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
 Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A. and Keele, J.W.
 Design and use of two pooled tissue normalized cDNA libraries for
 EST discovery in swine
 Unpublished (2000)
 On Jul 9, 1999 this sequence version replaced gi:5435515.

RESU T 9
AM436702 208 bp mRNA EST 14-FEB-2000
LOCUS: 77141 MARC 2Pig Sus scrofa cDNA 5', mRNA sequence.
DEFINITION: AM436702
ACCESSION: AM436702
VERSION: GI:6972008
KEYWORDS: EST.
SOURCE: Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
AUTHORS: Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heath, M.P., Grosse, W.M., Bennett, G.A. and Keeler, J.W.
TITLE: Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
JOURNAL: Unpublished (2000)
COMMENT: On Jul 9, 1999 this sequence version replaced gi:5435372.
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -mnscore 20 and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACAT
BACKWARD: GTTTCACACGACG
Plate: 32 row: E column: 18
Seq primer: ATTAGTGACACTATAG.
Location/Qualifiers
1..208
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_1lb="MARC 2Pig"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; site_1: xbaI; site_2: XhoI; library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT 36 a 64 c 73 g 35 t
ORIGIN
Query Match 9.5%; Score 167; DB 81; Length 208;
Best Local Similarity 87.9%; Pred. No. 1,2e-34;
Matches 182; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 1393 agcagcagagatgctcgcagccgagccacagatggggcgagagctggtctcttc 1452
DB 2 aacacacggggggcccccagacggcgctcacagctggggcgagctgacgacgtcttc 61
QY 1453 ttgggagatctcgacgacatccctgactctcatcttattgttgcgtcaagcagcagc 1512
DB 62 ctggggggttcttgacacatccctgactctcttctattgttgcgtcagcagcgacag 121
QY 1513 ccagcagaggaactcttgcttaagcagaagtggtgcctgagctggggcctcactctct 1572
DB 122 ccagcagaggaactcttgcttaagcagaagtggtgcctgagctggggcctcactctc 181
QY 1573 ggagaccacaagctacagcagaagacct 1599
DB 182 gggaccacacagctacagcagaagacct 208
RESULT 10 242773 212 bp mRNA EST 11-NOV-1994
LOCUS: 242773
DEFINITION: HSC07E021 normalized infant brain cDNA Homo sapiens cDNA clone
SOURCE: c-07e02, mRNA sequence.

ACCESSION 242773
VERSION 242773.1 GI:570345
KEYWORDS: EST.
SOURCE: human.
ORGANISM: Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE: 1 (bases 1 to 212)
Auffray, C., Behar, G., Bols, F., Bouchler, C., da Silva, C., Devignes, M.D., Duprat, S., Houligatte, R., Juneau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pletu, G., Pouillot, Y., Sebastiani-Kabakchis, C. and Tessier, A.
IMAGE: molecular integration of the analysis of the human genome and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
JOURNAL: Genexpress-Genethon
MEDLINE: Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, BP60 91002 Evry Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr
Single read.
Genexpress_library_idt: C; Genexpress_sequence_idt: y1c-07e02
Seq primer: (-21)M13-universal.
Location/Qualifiers
1..212
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="c-07e02"
/clone_1lb="normalized infant brain cDNA"
/sex="female"
/tissue_type="total brain"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII; Site_2: NotI; sex: female; dev_stage=3 months old; isolate=muscular atrophy patient; tissue_type=total brain; local mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector. Clone library from B.Souares, Psychiatry Dept. Columbia University, USA. Normalization_method: Bento Soares, P.N.A.S. in press"
BASE COUNT 48 a 56 c 58 g 45 t 5 others
ORIGIN
Query Match 8.0%; Score 141; DB 20; Length 212;
Best Local Similarity 97.6%; Pred. No. 1,2e-27;
Matches 163; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
QY 835 ctccacagcagcagtcgcagtcgagctcagctcagctcttgaagatctgacctatc 894
DB 28 ctccacagcagcagtcgcagtcgagctcagctcagctcttgaagatctgacctatc 86
QY 895 ccagagccacacagcttgaagacatgaatgttaccacagctgctcctgttggctcc 954
DB 87 ccagagccacacacagcttgaagacatgaatgttaccacagctgctcctgttggctcc 146
QY 955 cgtactgaagtgacacaaagtgaatacaacacactgtgctgcctca 1001
DB 147 cgtactgaagtgacacaaagtgaatacaacacactgtgctgcctca 192
RESULT 11
AM346693 232 bp mRNA EST 01-FEB-2000
LOCUS: AM346693
DEFINITION: 29273 MARC 1Pig Sus scrofa cDNA 5', mRNA sequence.
ACCESSION: AM346693
VERSION: AM346693.1 GI:6844403
KEYWORDS: EST.
SOURCE: Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE: 1 (bases 1 to 232)
Auffray, C., Behar, G., Bols, F., Bouchler, C., da Silva, C., Devignes, M.D., Duprat, S., Houligatte, R., Juneau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pletu, G., Pouillot, Y., Sebastiani-Kabakchis, C. and Tessier, A.
IMAGE: molecular integration of the analysis of the human genome and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
JOURNAL: Genexpress-Genethon
MEDLINE: Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, BP60 91002 Evry Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr
Single read.
Genexpress_library_idt: C; Genexpress_sequence_idt: y1c-07e02
Seq primer: (-21)M13-universal.
Location/Qualifiers
1..232
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="c-07e02"
/clone_1lb="normalized infant brain cDNA"
/sex="female"
/tissue_type="total brain"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII; Site_2: NotI; sex: female; dev_stage=3 months old; isolate=muscular atrophy patient; tissue_type=total brain; local mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector. Clone library from B.Souares, Psychiatry Dept. Columbia University, USA. Normalization_method: Bento Soares, P.N.A.S. in press"
BASE COUNT 48 a 56 c 58 g 45 t 5 others
ORIGIN

REFERENCE
AJ7 FORS
1 (bases 1 to 232)
Fehrenkrug, S.C., Fekling, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., and Keele, J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine

JOURNAL
COMMENT
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4356
Fax: 402 762 4390
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options.

PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCACGTCACGACG
Plate: 13 row: 1 column: 12
Seq primer: ATTAGGTGACACTATAG.

FEATURES
SOURCE
1..232
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1Pig"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site.1: XbaI; Site.2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."

BASE COUNT
37 a 65 c 80 g 50 t

ORIGIN

Query Match

Best Local Similarity 6.4%; Score 112.6; DB 80; Length 232;
Matches 118; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

1635 gccctggcgaagggagcagtgcttgctgagatctcacaccctctctgtatc 1694
|||||
1 GCCCTGGCCAGAGGGGCGAGTGTGCTGCTCCCTCCACCCCTCTGTCGATCC 60
Db
1695 ttgcacaaagccagccacatctggcttaactgggctctcttagccacatgtatgaac 1754
|||||
61 TTGCCGAGCCAGCCCATTCGCTGACGGGGCTCTCTAGCCACATGTGATGAAC 120
Db
1755 atccatc 1761
|||||
Db 121 GTCCATC 127

RESULT 12
AM346598 232 bp mRNA EST 01-FEB-2000
LOCUS
DEFINITION 29882 MARC 1Pig Sus scrofa cDNA 5', mRNA sequence.
ACCESSION AM346598
VERSION AM346598.1 GI:6844408
KEYWORDS EST.
SOURCE
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.

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EST discovery in swine

JOURNAL
COMMENT
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options.

PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCACGTCACGACG
Plate: 13 row: 1 column: 12
Seq primer: ATTAGGTGACACTATAG.

FEATURES
SOURCE
1..232
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1Pig"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site.1: XbaI; Site.2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."

BASE COUNT
37 a 65 c 78 g 52 t

ORIGIN

Query Match
Best Local Similarity 6.4%; Score 112.6; DB 80; Length 232;
Matches 118; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

1635 gccctggcgaagggagcagtgcttgctgagatctcacaccctctctgtatc 1694
|||||
1 GCCCTGGCCAGAGGGGCGAGTGTGCTGCTCCCTCCACCCCTCTGTCGATCC 60
Db
1695 ttgcacaaagccagccacatctggcttaactgggctctcttagccacatgtatgaac 1754
|||||
61 TTGCCGAGCCAGCCCATTCGCTGACGGGGCTCTCTAGCCACATGTGATGAAC 120
Db
1755 atccatc 1761
|||||
Db 121 GTCCATC 127

RESULT 13
AI365650 490 bp mRNA EST 07-JAN-1999
LOCUS
DEFINITION ap20108.x1 Schiller oligodendrogloma Homo sapiens cDNA clone
IMAGE:195967 3' similar to TR:062179 Q62179 SEMAPHORIN C ; , mRNA
sequence.
ACCESSION AI365650
VERSION AI365650.1 GI:4125339
KEYWORDS EST.
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 490)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Giesel, G., Jost, S.,
Kizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marz, M.,
Martin, D., Moore, B., Schenleberg, K., Steptoe, M., Tan, F.,
Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
The Human Genome Project
Unpublished (1997)
On May 1, 1998 this sequence version replaced gi:2339580.
JOURNAL
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found

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